



SEQUENCE LISTING

<110> Hilton, Douglas J.
Nicola, Nicos A.
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Wilson, Tracy
Zhang, Jian-Guo
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Rakar, Steven
Fabri, Louis
Kojima, Tetsuo
Maeda, Masatsugu
Kikuchi, Yasufumi
Nash, Andrew

<120> A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

<140> 09/037,657
<141> 1998-03-10

<150> 08/928,720
<151> 1997-09-11

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<170> PatentIn Ver. 2.0

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cccccgccagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgccacc 120

ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 168
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
1 5 10 15

ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tct tgt gtc 216
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
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ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
Leu Gly Val Pro Arg Gly Ser Gly Ala His Thr Ala Val Ile Ser
35 40 45

ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
50 55 60

tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
65 70 75

acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
80 85 90 95

acc tcc acc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
Thr Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
100 105 110

cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
115 120 125

gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
130 135 140

atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr

145	150	155	
ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	160 165	170	648
tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	180	185 190	696
act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe	195	200	744
act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala	210	215	792
aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp	225	230 235	840
ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln	240	245	888
ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe	260	265	936
caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp	275	280	984
aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	290	295	1032
ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	305	310	1080
ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His	320	325	1128
ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly	340	345	1176
ggg gtg tgc gag ccg cgg ggc gag ccc agc tcg ggc ccg gtg cgg Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg	355	360	1224
cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys	370	375	1272
tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln	385	390	1320
aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc			1362

Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu													
400	405		410	taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct	1422	ctgtaccatc tggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa	1482	ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg	1542	ggtattgcag gcctcccaa caatctttt aaataaataa aggagttgtt caggtaaaaaa	1602	aaaaaaaaaa aaaaaaaaaa aaaaaaaa	1629
	410												
taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct	1422												
ctgtaccatc tggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa	1482												
ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg	1542												
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	10	15																																																																					
Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu																																																																							
20	25	30																																																																					
Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro																																																																							
35	40	45																																																																					
Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser																																																																							
50	55	60																																																																					
Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr																																																																							
65	70	75	80																																																																				
Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr																																																																							
85	90	95																																																																					
Ser Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln Gln																																																																							
100	105	110																																																																					
Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala																																																																							
115	120	125																																																																					
Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile																																																																							
130	135	140																																																																					
Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro																																																																							
145	150	155	160																																																																				
Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr																																																																							
165	170	175																																																																					
Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr																																																																							
180	185	190																																																																					
Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr																																																																							
195	200	205																																																																					
Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg																																																																							
210	215	220																																																																					

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
 225 230 235 240
 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
 245 250 255
 Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
 260 265 270
 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
 290 295 300
 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
 305 310 315 320
 Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
 325 330 335
 Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
 340 345 350
 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
 355 360 365
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
 370 375 380
 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
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 <222> (125)..(1399)

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 cccaaatg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 169
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 1 5 10 15
 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 217
 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
 20 25 30

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Leu	Gly	Val	Pro	Arg	Gly	Gly	Ser	Gly	Ala	His	Thr	Ala	Val	Ile	Ser	
35							40						45			
ccc	cag	gac	ccc	acc	ctt	ctc	atc	ggc	tcc	tcc	ctg	caa	gct	acc	tgc	313
Pro	Gln	Asp	Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	
50							55				60					
tct	ata	cat	gga	gac	aca	cct	ggg	ggc	acc	gct	gag	ggg	ctc	tac	tgg	361
Ser	Ile	His	Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	
65							70				75					
acc	ctc	aat	ggt	cgc	cgc	ctg	ccc	tct	gag	ctg	tcc	cgc	ctc	ctt	aac	409
Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	
80							85			90			95			
acc	tcc	acc	ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	457
Thr	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	
							100			105			110			
cag	tca	gga	gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	505
Gln	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	
							115			120			125			
gct	ggc	tcc	tgc	ctc	tat	gtt	ggc	ttg	ccc	cct	gag	aag	ccc	ttt	aac	553
Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	
							130			135			140			
atc	agc	tgc	tgg	tcc	cg	aa	atg	aag	gat	ctc	acg	tgc	cgc	tgg	aca	601
Ile	Ser	Cys	Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	
							145			150			155			
ccg	gg	gca	cac	gg	gag	aca	ttc	tta	cat	acc	aa	tac	tcc	ctc	aag	649
Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	
							160			165			170			
tac	aag	ctg	agg	tgg	tac	gg	cag	gat	aa	aca	tgt	gag	gag	tac	cac	697
Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	
							180			185			190			
act	gt	ggc	cct	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	tcc	745
Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	
							195			200			205			
act	ccc	tat	gag	atc	tgg	gt	gaa	gg	acc	aa	cgc	cta	ggc	tca	gca	793
Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	
							210			215			220			
aga	tct	gat	gtc	ctc	aca	ctg	gat	gtc	ctg	gac	gt	gt	acc	acg	gac	841
Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	
							225			230			235			
ccc	cca	ccc	gac	gt	cac	gt	agc	cgc	gtt	gg	gg	ctg	gag	gac	cag	889
Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	
							240			245			250			
ctg	agt	gt	cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	tcc	ctc	tcc	937
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	
							260			265			270			
caa	gcc	aag	tac	cag	atc	cgc	tac	cgc	gt	gag	gac	agc	gt	gac	tgg	985
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
							275			280			285			

aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc	1033
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	
290 295 300	
ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgc aac cca ttc	1081
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	
305 310 315	
ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac	1129
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His	
320 325 330 335	
ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc	1177
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly	
340 345 350	
ggg gtg tgc gag ccg cgg ggc gag ccc agc tcg ggc ccg gtg cgg	1225
Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg	
355 360 365	
cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc	1273
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys	
370 375 380	
tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag	1321
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln	
385 390 395	
aag tca cac aag acc cga aac cag gac gag ggg atc ctg cct tcg ggc	1369
Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly	
400 405 410 415	
aga cgg ggt gcg gcg aga ggt cct gcc ggt taaaactctaa ggataggcca	1419
Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly	
420 425	
tcctcctgct gggtcagacc tggaggctca cctgaattgg agcccctctg taccatctgg	1479
gcaacaaaga aacctaccag aggctggggc acaatgagct cccacaacca cagtttggt	1539
ccacatgatg gtcacacttg gatatacccc agtgtggta aggttgggtt attgcaggc	1599
ctccccacaa tctctttaaa taaataaagg agttgttcag gtaaaaaaaaaaaaaaa	1659
aaaaaaaaaaa aaaa	1673

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<220>
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 20 25 30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
 50 55 60
 Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
 65 70 75 80
 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
 85 90 95
 Ser Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln Gln
 100 105 110
 Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
 115 120 125
 Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
 130 135 140
 Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
 145 150 155 160
 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
 165 170 175
 Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
 180 185 190
 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
 195 200 205
 Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
 210 215 220
 Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
 225 230 235 240
 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
 245 250 255
 Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
 260 265 270
 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
 290 295 300
 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
 305 310 315 320
 Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
 325 330 335
 Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
 340 345 350
 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
 355 360 365
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
 370 375 380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
 385 390 395 400

Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
 405 410 415

Arg Gly Ala Ala Arg Gly Pro Ala Gly
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 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1 5 10 15

ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac ccc acc gct 96
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
 20 25 30

gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc ggg gtg tgc 144
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys
 35 40 45

gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg cgc gag ctc 192
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
 50 55 60

aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc tcg aac ctt 240
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65 70 75 80

agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag aag tca cac 288
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
 85 90 95

aag acc cga aac cag gta gga aag ttg ggg gag gct tgc gtg ggg ggt 336
 Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
 100 105 110

aaa gga gca gag gaa gag aga gac ccg ggt gag cag cct cca caa cac 384
 Lys Gly Ala Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
 115 120 125

cgc act ctt ctt tcc aag cac agg acg agg gga tcc tgc cct cgg gca 432
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
 130 135 140

gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
 145 150 155

ctagatgagg ccctttcccc tccttcggtg ttgctcaaag ggatctctta gtgctcattt 545
cacccactgc aaagagcccc aggtttact gcatcatcaa gttgctgaag ggtccaggct 605
taatgtggcc tctttctgc cctcaggtcc tgccggctaa actctaagga taggccatcc 665
tcctgctggg tcagacctgg aggctcacct gaattggagc ccctctgtac ctatctggc 725
aacaaaagaaa cctaccatga ggctggggca caatgagctc ccacaaccac agctttggc 785
cacatgatgg tcacacactgg atataccca gtgtggtaa ggttgggta ttgcaggcc 845
tcccaacaat ctctttaat aaataaagga gttgttcagg taaaaaaaaa aaaaaaaaaa 905
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 938

<210> 17
<211> 155
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6.3

<400> 17
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
1 5 10 15
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
20 25 30
Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys
35 40 45
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
50 55 60
Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
65 70 75 80
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
85 90 95
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly
100 105 110
Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
115 120 125
Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
130 135 140
Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145 150 155

<210> 18
<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(834)

<220>
<223> Description of Artificial Sequence: Nucleotide sequence of products generated by 5' RACE of brain cDNA using NR6 specific primers

<400> 18																		48
ccc	acc	ctt	ctc	atc	ggc	tcc	tcc	ctg	caa	gct	acc	tgc	tct	ata	cat			
Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	Ser	Ile	His			
1				5					10					15				
gga	gac	aca	cct	ggg	gcc	acc	gct	gag	ggg	ctc	tac	tgg	acc	ctc	aat			96
Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	Thr	Leu	Asn			
			20					25					30					
ggt	cgc	cgc	ctg	ccc	tct	gag	ctg	tcc	cgc	ctc	ctt	aac	acc	tcc	acc			144
Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	Thr	Ser	Thr			
			35				40					45						
ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	cag	tca	gga			192
Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln	Ser	Gly			
			50			55					60							
gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	gct	ggc	tcc			240
Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala	Gly	Ser			
			65			70				75					80			
tgc	ctc	tat	gtt	ggc	ttg	ccc	cct	gag	aag	ccc	ttt	aac	atc	agc	tgc			288
Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Cys			
				85				90					95					
tgg	tcc	cgg	aac	atg	aag	gat	ctc	acg	tgc	cgc	tgg	aca	ccg	ggt	gca			336
Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala			
			100				105						110					
cac	ggg	gag	aca	ttc	tta	cat	acc	aac	tac	tcc	ctc	aag	tac	aag	ctg			384
His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu			
			115				120					125						
agg	tgg	tac	ggt	cag	gat	aac	aca	tgt	gag	gag	tac	cac	act	gtg	ggg			432
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Gl	Gl	Tyr	His	Thr	Val	Gly			
			130			135					140							
ccc	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	ttc	act	ccc	tat			480
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr			
				145		150				155					160			
gag	atc	tgg	gtg	gaa	gcc	acc	aat	cgc	cta	ggc	tca	gca	aga	tct	gat			528
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp			
				165				170					175					
gtc	ctc	aca	ctg	gat	gtc	ctg	gac	gtg	gtg	acc	acg	gac	ccc	cca	ccc			576
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro			
			180				185						190					
gac	gtg	cac	gtg	agc	cgc	gtt	ggg	ggc	ctg	gag	gac	cag	ctg	agt	gtg			624
Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val			
			195				200					205						
cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	ttc	ctc	ttc	caa	gcc	aag			672
													13					

Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys	
210						215					220					
tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	aag	gtg	gtg	720
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val	
225						230					235					240
gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	ctg	aag	ccc	768
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro	
						245				250					255	
ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	ggg	atc	tat	816
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr	
						260			265				270			
ggg	tcg	aaa	aag	gcg	gga											834
Gly	Ser	Lys	Lys	Ala	Gly											
						275										

<210> 19
 <211> 278
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Haemopoietin receptor

<400> 19																
Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	Ser	Ile	His	
1				5					10					15		
Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	Thr	Leu	Asn	
								20	25				30			
Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	Thr	Ser	Thr	
								35	40				45			
Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln	Ser	Gly	
						50		55				60				
Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala	Gly	Ser	
					65			70			75			80		
Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Cys	
					85				90					95		
Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala	
					100			105				110				
His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	
					115			120			125					
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly	
					130			135			140					
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr	
					145			150			155			160		
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp	
					165				170			175				
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro	
					180			185				190				

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
 195 200 205
 Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
 210 215 220
 Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
 225 230 235 240
 Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
 245 250 255
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 260 265 270
 Gly Ser Lys Lys Ala Gly
 275

<210> 20
 <211> 143
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (105)..(143)

<220>
 <223> Description of Artificial Sequence:Nucleotide
 sequence unique to 5' RACE of brain cDNA

<400> 20
 ggcatgaagg cttagggtgg ggatcgtag gacccatgca cccagagaaa gggactgg 60
 gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116
 Met Asn Gly Leu
 1

aga cac agc tgt aat cag ccc cca gga 143
 Arg His Ser Cys Asn Gln Pro Pro Gly
 5 10

<210> 21
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Amino Acid Sequence encoded by Nucleotide
 sequence unique to 5' RACE of brain cDNA

<400> 21
 Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
 1 5 10

<210> 22
 <211> 1930
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown Organism:Murine NR6

<400> 22

ggcacagact tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60
ccccgcagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
ccaaatgccc gcgggtcgcc cggggcccggt cgcccaatcc gcgcggcggc cgccgcccggcc 180
gctgtccctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240
gggagcccac acagctgtaa tcagcccca ggacccacc cttctcatcg gctcctccct 300
gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360
gaccctcaat ggtcgccgccc tgccctctga gctgtcccgcc ctcccttaaca cctccaccct 420
ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctgggttg 480
tcacgcccga gacggcagca ttctggctgg ctccctgcctc tatgttgct tgcccccgtga 540
gaagcccttt aacatcagct gctggtcccgg gaacatgaag gatctcacgt gccgctggac 600
accgggtgca cacggggaga cattttaca taccaactac tccctcaagt acaagctgag 660
gtggtacggt caggataaca catgtgagga gtaccacact gtggggccctc actcatgcca 720
tatccccaaag gacctggccc tcttcactcc ctatgagatc tgggtggaag ccaccaatcg 780
cctaggctca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840
ccccccaccc gacgtgcacg tgagccgcgt tggggccctg gaggaccagc tgagtgtgcg 900
ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaagtacc agatccgcta 960
ccgcgtggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctccctg 1020
ccgtctcgcg ggcctgaagc ccggcaccgt ttacttcgtc caagtgcgtt gtaaccatt 1080
cgggatctat gggtcgaaaa aggccggaaat ctggagcag tggagccacc ccaccgctgc 1140
ctccacccct cgaagtgagc gccccggccc gggcggcggg gtgtgcgagc cgccggggcgg 1200
cgagcccagc tcgggcccgg tgcggcgcga gctcaagcag ttccctggct ggctcaagaa 1260
gcacgcatac tgctcgaacc ttagttccg cctgtacgac cagtggcgtg cttggatgca 1320
gaagtcacac aagacccgaa accaggtagg aaagttgggg gaggctgcg tgggggtaa 1380
aggagcagag gaagagagag accccgggtga gcagcctcca caacaccgca ctcttccttc 1440
caagcacagg acgaggggat cctgcccctcg ggcagacggg gtgcggcggag aggtaaagggg 1500
gtctgggtga gtggggcccta cagcagtcta gatgaggccc tttccctcc ttcgggtttg 1560
ctcaaaggga tctcttagtg ctcatttcac ccactgc当地 gagcccccagg ttttactgca 1620
tcatcaagtt gctgaagggt ccaggctaa tgtggccctt tttctgc当地 caggtcctgc 1680
cggtctaaact ctaaggatag gccatcctcc tgctgggtca gacccggagg ctcacccgtaa 1740
ttggagccccc tctgtaccta tctggcaac aaagaaacct accatgaggc tggggcacaa 1800

tgagctccca caaccacagc tttggtccac atgatggtca cacttggata taccccaagt 1860
tgggtaaggt tgggttattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920
gttcaggtaa 1930

<210> 23
<211> 560
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR product for
human NR6

<400> 23
tccaggcagc ggtcgaaaaa caacccgtg tgccacgccc gtgacggcag catcctggct 60
ggctcctgcc tctatgttgg cctgccccca gagaaacccg tcaacatcag ctgctggtcc 120
aagaacatga aggacttgac ctgcccgtgg acgccagggg cccacgggaa gaccccttc 180
cacaccaact actccctcaa gtacaagctt aggtggatg gccaggacaa cacatgtgag 240
gagtaccaca cagtggggcc ccactcctgc cacatccccca aggacctggc tctcttacg 300
ccctatgaga tctgggtgga ggccaccaac cgcctgggct ctgcccgtc cgatgtactc 360
acgctggata tcctggatgt ggtgaccacg gaccccccgc ccgacgtgca cgtgagccgc 420
gtcgaaaaa tggaggacca gctgagcgtg cgctgggtgt cgccacccgc cctcaaggat 480
ttcccttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540
gtggtggacg atgtgagcaa 560

<210> 24
<211> 1391
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)..(1050)

<220>
<223> Description of Unknown Organism:Nucleotide
sequence of clone HFK-66 encoding human NR6

<400> 24
acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac 48
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
1 5 10 15
gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag 96
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
20 25 30
cggtcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg 144
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
35 40 45

gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag aaa ccc gtc aac	192
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn	
50 55 60	
atc agc tgc tgg tcc aag aac atg aag gac ttg acc tgc cgc tgg acg	240
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
65 70 75 80	
cca ggg gcc cac ggg gag acc ttc ctc cac acc aac tac tcc ctc aag	288
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
85 90 95	
tac aag ctt agg tgg tat ggc cag gac aac aca tgt gag gag tac cac	336
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
100 105 110	
aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac ctg gct ctc ttt	384
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe	
115 120 125	
acg ccc tat gag atc tgg gtg gag gcc acc aac cgc ctg ggc tct gcc	432
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala	
130 135 140	
cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg gtg acc acg gac	480
Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp	
145 150 155 160	
ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc ctg gag gac cag	528
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln	
165 170 175	
ctg agc gtg cgc tgg gtg tcg cca ccc gcc ctc aag gat ttc ctc ttt	576
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe	
180 185 190	
caa gcc aaa tac cag atc cgc tac cga gtg gag gac agt gtg gac tgg	624
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp	
195 200 205	
aag gtg gtg gac gat gtg agc aac cag acc tcc tgc cgc ctg gcc ggc	672
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	
210 215 220	
ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc tgc aac ccc ttt	720
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	
225 230 235 240	
ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt gag tgg agc cac	768
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His	
245 250 255	
ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg ggc ccg ggc ggc	816
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly	
260 265 270	
ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tcg ggg ccg gtg cgg	864
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg	
275 280 285	
cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag cac gcg tac tgc	912
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys	
290 295 300	

tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga gcc tgg atg cag	960
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln	
305 310 315 320	
aag tcg cac aag acc cgc aac cag cac agg acg agg gga tcc tgc cct	1008
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro	
325 330 335	
cgg gca gac ggg gca cgg cga gag gtc ctg cca gat aag ctg	1050
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu	
340 345 350	
taggggctca ggccaccctc cctgccacgt ggagacgcag agggcgaacc caaactgggg	1110
ccacctctgt accctcaactt cagggcacct gagccctca gcaggagctg gggtggccccc	1170
ttagctccaa cggccataac agctctgact cccacgtgag gccaccttg ggtgcacccc	1230
agtgggtgtg tgtgtgtgtg tgagggttgg ttgagttgcc tagaaccctt gccagggctg	1290
ggggtgagaa ggggagtcata tactccccat tacctaggc ccctccaaaa gagtcctttt	1350
aaataaatga gctatttagg tgcaaaaaaa aaaaaaaaaa a	1391

<210> 25
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Haemopoietin receptor

Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn	
1 5 10 15	
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln	
20 25 30	
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu	
35 40 45	
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn	
50 55 60	
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
65 70 75 80	
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
85 90 95	
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
100 105 110	
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe	
115 120 125	
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala	
130 135 140	
Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp	
19	

145	150	155	160
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln			
165		170	175
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe			
180	185		190
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp			
195	200	205	
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly			
210	215	220	
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe			
225	230	235	240
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His			
245	250	255	
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly			
260	265	270	
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg			
275	280	285	
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys			
290	295	300	
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln			
305	310	315	320
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro			
325	330	335	
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu			
340	345	350	

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:UP1
 Oligonucleotide

<400> 26
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<210> 27
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 <213> Artificial Sequence

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<223> Description of Unknown Organism:Murine NR6 gene

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<213> Unknown

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<223> Description of Unknown Organism:Murine NR6

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<222> (139)

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35 40 45
Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln Gln Ser
50 55 60
Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly
65 70 75 80
Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
85 90 95
Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly
100 105 110
Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys
115 120 125
Leu Arg Leu Val Arg Ser Glu Xaa His Met Xaa Gly Val Pro His Cys
130 135 140
Glu Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser
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<210> 31
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<212> DNA
<213> Artificial Sequence

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 <213> Artificial Sequence

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 <212> PRT
 <213> Artificial Sequence

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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:3' UTR
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73

<210> 36
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27

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gggggtgggggg ga 11832

<210> 39
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Murine peptide

<400> 39
Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln
1 5 10 15

Ala Thr Cys Ser Ile His Gly Asp Thr Pro
20 25

<210> 40
<211> 21
<212> DNA
<213> Oligonucleotide Sequence

<400> 40

gtccaaagtgc gttgttaaccc a 21

<210> 41
<211> 24
<212> DNA
<213> Oligonucleotide Sequence

<400> 41

gctgagtggtg cgctgggtct cacc 24

<210> 42
<211> 18
<212> DNA
<213> Oligonucleotide Sequence

<400> 42

ggctccactc gctccaga 18

<210> 43
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (513)..(1775)

<220>
<223> Description of Unknown Organism: Nucleotide Sequence of NR6

<400> 43
gcggattttg tgtttcaaat ctatctacag aaaagattga gaaccagaag ccctttcgt 60

tttttgaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgtt 120

gactgcagtg tcagggatcc aaaggaaatg actccatccc ttccctttca tcccaacctc 180

agtgacagca aattctgtatg tgactgaggg ttggcttgc aaggagtcat tagaaattc 240

tgcctaaagcc atagcgcgat gagaaggatg tattctatgg tgggtatttt cctgtcccc 300

ctcagaggaa agttgtcaga tgagcaggatg gagtattcta tagcaaacag caagctaata 360

ggttacacag ataactctct gacttgcct tacagaacct gtgttattga ccttagggca 420
 aggttcatgc tcagggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct 480
 catatttcag cgccccggc agcgccggcc cc atg ccc gcc ggc cgc cgg ggc 533
 Met Pro Ala Gly Arg Arg Gly
 1 5
 ccc gcc gcc caa tcc gcg cgg ccg ccg ttg ctg ccc ctg ctg 581
 Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu
 10 15 20
 ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca 629
 Leu Leu Cys Val Leu Gly Ala Pro Arg Ala Gly Ser Gly Ala His Thr
 25 30 35
 gct gtg atc agt ccc cag gat ccc acg ctt ctc atc ggc tcc tcc ctg 677
 Ala Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu
 40 45 50 55
 ctg gcc acc tgc tca gtg cac gga gac cca cca gga gcc acc gcc gag 725
 Leu Ala Thr Cys Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu
 60 65 70
 ggc ctc tac tgg acc ctc aat ggg cgc cgc ctg ccc cct gag ctc tcc 773
 Gly Leu Tyr Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser
 75 80 85
 cgt gta ctc aac gcc tcc acc ttg gct,ctg gcc ctg gcc aac ctc aat 821
 Arg Val Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Asn Leu Asn
 90 95 100
 ggg tcc agg cag cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac 869
 Gly Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
 105 110 115
 ggc agc atc ctg gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag 917
 Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu
 120 125 130 135
 aaa ccc gtc aac atc agc tgc tgg tcc aag aac atg aag gac ttg acc 965
 Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr
 140 145 150
 tgc cgc tgg acg cca ggg gcc cac ggg gag acc ttc ctc cac acc aac 1013
 Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn
 155 160 165
 tac tcc ctc aag tac aag ctt agg tgg tat ggc cag gac aac aca tgt 1061

Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys			
170	175	180	
gag gag tac cac aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac		1109	
Glu Glu Tyr His Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp			
185	190	195	
ctg gct ctc ttt acg ccc tat gag atc tgg gtg gag gcc acc aac cgc		1157	
Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg			
200	205	210	215
ctg ggc tct gcc cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg		1205	
Leu Gly Ser Ala Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val			
220	225	230	
gtg acc acg gac ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc		1253	
Val Thr Thr Asp Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly			
235	240	245	
ctg gag gac cag ctg agc gtg cgc tgg gtg tcg cca ccc gcc ctc aag		1301	
Leu Glu Asp Gln Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys			
250	255	260	
gat ttc ctc ttt caa gcc aaa tac cag atc cgc tac cga gtg gag gac		1349	
Asp Phe Leu Phe Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp			
265	270	275	
agt gtg gac tgg aag gtg gtg gac gat gtg agc aac cag acc tcc tgc		1397	
Ser Val Asp Trp Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys			
280	285	290	295
cgc ctg gcc ggc ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc		1445	
Arg Leu Ala Gly Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg			
300	305	310	
tgc aac ccc ttt ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt		1493	
Cys Asn Pro Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser			
315	320	325	
gag tgg agc cac ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg		1541	
Glu Trp Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro			
330	335	340	
ggc ccg ggc ggc ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tcg		1589	
Gly Pro Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser			
345	350	355	
ggg ccg gtg cgg cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag		1637	
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys			
360	365	370	375
cac gcg tac tgc tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga		1685	

His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg		
380	385	390
gcc tgg atg cag aag tcg cac aag acc cgc aac cag gac gag ggg atc		1733
Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile		
395	400	405
ctg ccc tcg ggc aga cgg ggc acg gcg aga ggt cct gcc aga		1775
Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg		
410	415	420
taagctgtag gggctcaggc caccctccct gccacgtgga gacgcagagg ccgaacccaa 1835		
actggggcca cctctgtacc ctcacttcag ggcacctgag ccaccctcag caggagctgg 1895		
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atcc		2079

<210> 44
 <211> 421
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Amino Acid Sequence of NR6

<400> 44			
Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg Pro			
1	5	10	15
Pro Pro Leu Leu Pro Leu Leu Leu Cys Val Leu Gly Ala Pro Arg			
20	25	30	
Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro Gln Asp Pro Thr			
35	40	45	
Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys Ser Val His Gly Asp			
50	55	60	
Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn Gly Arg			
65	70	75	80
Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn Ala Ser Thr Leu Ala			
85	90	95	
Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Arg Ser Gly Asp Asn			
100	105	110	
Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser Cys Leu			
115	120	125	

Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn Ile Ser Cys Trp Ser
 130 135 140
 Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly
 145 150 155 160
 Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp
 165 170 175
 Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His
 180 185 190
 Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile
 195 200 205
 Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
 210 215 220
 Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp Val
 225 230 235 240
 His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val Arg Trp
 245 250 255
 Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys Tyr Gln
 260 265 270
 Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val Asp Asp
 275 280 285
 Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro Gly Thr
 290 295 300
 Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr Gly Ser
 305 310 315 320
 Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala Ala Ser
 325 330 335
 Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Ala Cys Glu Pro
 340 345 350
 Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu Lys Gln
 355 360 365
 Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu Ser Phe
 370 375 380
 Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr
 385 390 395 400
 Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala
 405 410 415
 Arg Gly Pro Ala Arg
 420

<210> 45
 <211> 23
 <212> DNA
 <213> Artificial

<220>

<223> Description of Artificial sequence: Fwd Primer

<400> 45
tgcccccaga gaaacccgtc aac

23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Rev Primer

<400> 46
cgtgagtaca tcggagcggg cagag

25

<210> 47
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 47
tcaggcgcbc cttgcccaca cagctgtat c

31

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 48
tcaggcgcbc ctttatctgg caggacctct

30

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 49
tcaggcgcbc ctgcccggccg gcccgc

25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 50
ataaggcgcg ccctggcagg acctctcg 28

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 51
tcaggcgcbc cttgcccaca cagctgtat c 31

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 52
tcaggcgcg ccttatctgg caggacctct 30

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 53
tcaggcgcbc ctgccccccg gcccgc 25

<210> 54
<211> 28
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 54
ataaggcgcg ccctggcagg acctctcg 28

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide

<400> 55

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 56
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 56
ctagactagt gctgacacaa tggttcttgc cagctctacc accagcatcc acaccatgct 60
gctcctgctc ctgatgctct tccacctggg actccaagct tcaatctgg cgccgcagga 120
ctacaaggac gacgatgaca agacgcgtgc tagcactagt 160

<210> 57
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 57
ctagactagt gctagcacgc gtcttgtcat cgtcgtcctt gtagtcctgg cgccgcgaga 60
ttgaagcttg gagtcccagg tggaagacga tcaggagcag gagcagcatg gtgtggatgc 120
tggtgtttaga gctggcaaga accattgtgt cagcactagt 160

<210> 58
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 58
aataaataaa 10